Amendments to the Specification

Please amend paragraph [0071] that extends from page 27 to page 28 as follows:

[0071] F is a fragment match, *i.e.* the match restricted to what concerns the fragments. Typically, when a peptide match is observed, the theoretical MS/MS spectrum is computed with possible modifications W included to match the peptide mass. See Baker & Clauser (Baker, P. and Clauser, K. *MS-Product*, part of the Protein Prospector suite at world wide web address ~~http://prospector.ucsf.edu/~~ prospector.ucsf.edu/) for theoretical MS/MS spectrum computation. The fragment match is then composed of the experimental fragment masses that are close enough to theoretical fragment masses:

$$F = \{(f_j, \text{int}(f_j), \text{series}(f_j), \text{pos}(f_j), m_{t,j})\},\ j \in J$$

where J is a set of indices used for indexing the experimental fragment masses f_j that are close enough to a theoretical fragment mass. Assuming that $m_{t,j}$ is the theoretical fragment mass; hence an experimental mass f_j is close enough to a theoretical mass if $|f_j - m_{t,j}| \leq D_f$ or, in case we give the tolerance in ppm, if $10^6 \mid f_j - m_{t,j} \mid / (0.5(f_j + m_{t,j})) \leq D_f$ or, in case of a non-symmetric tolerance, $f_j \in D_f(m_{t,j})$. The theoretical mass $m_{t,j}$ corresponds to the amino acid at position $\text{pos}(f_j)$ in the peptide sequence and ion series $\text{series}(f_j) \in S$. The intensity of the experimental signal f_j is $\text{int}(f_j)$. See Tables 3 and 4 for an example. The theoretical MS/MS spectrum of a peptide depends on the ion series (S) and on the peptide modifications (W), then F is written as $F(D_f,S,W)$. The information about intensity contained in tuple F may be removed. The information per individual fragment may be augmented by extra information provided by the signal processing software (peak detection) like peak width, signal to noise, quality of fit with a peptide signal theoretical pattern, etc. Hence a more complete version of F is

$$F = \{(f_j, \text{int}(f_j), \text{width}(f_j), \text{sn}(f_j), \text{fit}(f_j), \text{series}(f_j), \text{pos}(f_j), m_{t,j})\},\ j \in J.$$